

**REMARKS**

Justification for the amendments is as follows. Claims 2, 3, and 11-13 are canceled above, and claims 1, 4-10, and 14-18 are pending.

The amendment to the specification at pages 35 through 43 of the specification replaces the Sequence Listing as filed with the Substitute Sequence Listing filed December 11, 1997, in prior U.S. application Serial No. 08/567,508, and referenced in the filing papers for the present application. (See page 1 of the transmittal for the present application.) The Substitute Sequence Listing properly identifies the MUSPTK1 sequence, described at page 5 of the specification and shown in Figures 2A, 2B, 2C, 2D, 2E, and 2F as originally filed, as SEQ ID NO:3, and identifies sequences XLR and XLF, which appear at page 21 of the specification as originally filed, as SEQ ID NO:4 and SEQ ID NO:5, respectively. These sequences do not constitute new matter as MUSPTK1, XLR, and XLF appear in the application as filed.

The Substitute Sequence Listing corrects an error in SEQ ID NO:2 in the Sequence Listing as originally filed. Specifically, the latter part of SEQ ID NO:2, starting around residue 990, appears to have been incorrectly translated. However, SEQ ID NO:2 was correct as shown in Figures 1A, 1B, 1C, 1D, 1E, and 1F as filed. Accordingly, SEQ ID NO:2 as it appears in the Substitute Sequence Listing accompanying this Amendment is correct. This corrected sequence is not new matter as the correct sequence was shown in Figures 1A, 1B, 1C, 1D, 1E, and 1F of the application as filed. Applicants apologize for any inconvenience that might have been caused by this error. Applicants note that SEQ ID NO:1 was correct in the application as filed in both Figures 1A, 1B, 1C, 1D, 1E, and 1F and in the Sequence Listing.

The amendments to the specification at page 5, lines 2 and 6, and page 20, line 24, are made to reflect the renumbering of the figures in the preparation of formal drawings. The remaining amendments to the specification are merely typographical or grammatical in nature.

The amendments to the drawings were made to clarify Figures 2A, 2B, 2C, 2D, and 2E, and 2F. Specifically, Figures 2A, 2B, 2C, 2D, 2E, and 2F as originally filed showed the alignment between HJAK2 (SEQ ID NO:2) and MUSPTK1 (GI 409584; SEQ ID NO:3), along with two consensus sequences generated by DNASTAR software, the multisequence alignment program used. Figures 2A, 2B, 2C, 2D, 2E, and 2F as amended show only the alignment

between HJAK2 (SEQ ID NO:2) and MUSPTK1 (GI 409584; SEQ ID NO:3).

No new matter is added by any of these amendments.

If there are any questions regarding the above, the Examiner is invited to call Applicants' Agent at (650) 855-0555.

Respectfully submitted,

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~~M G M A C L T M T E M E T S T S . . . Q N G D I . G . A N~~  
~~M G M A C L T M T E M E G T S T S S V H Q N G D I S G S A N~~  
10 20 30  
1 **M G M A C L T M T E M E A T S T S P V H Q N G D I P G S A N**  
1 **M G M A C L T M T E M E G T S T S S I Y Q N G D I S G N A N**

~~S . K Q I . P V L Q V Y L Y H S L G . . . E . . . Y L . F P S G~~  
~~S V K Q I D P V L Q V Y L Y H S L G Q A E G D Y L T F P S G~~  
40 50 60  
31 **S V K Q I E P V L Q V Y L Y H S L G Q A E G E Y L K P P S G**  
31 **S M K Q I D P V L Q V Y L Y H S L G K S E A D Y L T F P S G**

~~E Y V . E E I C . A A S K A C G I T P V Y H N M F A L M S E~~  
~~E Y V G E E I C V A A S K A C G I T P V Y H N M F A L M S E~~  
70 80 90  
61 **E Y V A E E I C V A A S K A C G I T P V Y H N M F A L M S E**  
61 **E Y V G E E I C I A A S K A C G I T P V Y H N M F A L M S E**

~~T E R I W Y P P N H V F H I D E S T R H . . . L Y R I R F Y F~~  
~~T E R I W Y P P N H V F H I D E S T R H D V L Y R I R F Y F~~  
100 110 120  
91 **T E R I W Y P P N H V F H I D E S T R H D I L Y R I R F Y F**  
91 **T E R I W Y P P N H V F H I D E S T R H N V L Y R I R F Y F**

~~P . W Y C S G S . R . Y R . G . S R G A E A P L L D D F V M~~  
~~P H W Y C S G S S R A Y R H G V S R G A E A P L L D D F V M~~  
130 140 150  
121 **P H W Y C S G S S R T Y R Y G V S R G A E A P L L D D F V M**  
121 **P R W Y C S G S N R A Y R H G I S R G A E A P L L D D F V M**

~~S Y L F . Q W R H D F V H G W I K V P V T H E T Q E E C L G~~  
~~S Y L F A Q W R H D F V H G W I K V P V T H E T Q E E C L G~~  
160 170 180  
151 **S Y L F V Q W R H D F V H G W I K V P V T H E T Q E E C L G**  
151 **S Y L F A Q W R H D F V H G W I K V P V T H E T Q E E C L G**

~~M . V L D M M R I A K E . D Q T P L A . Y N S . S Y K T F L~~  
~~M A V L D M M R I A K E N D Q T P L A V Y N S V S Y K T F L~~  
190 200 210  
181 **M A V L D M M R I A K E K D Q T P L A V Y N S V S Y K T F L**  
181 **M T V L D M M R I A K E N D Q T P L A I Y N S I S Y K T F L**

FIGURE 2A

~~P C R A K I Q D Y H I L T R K R I R Y R F R R F I Q Q F~~  
~~P Q C V R A K I Q D Y H I L T R K R I R Y R F R R F I Q Q F~~  
220 230 240  
211 **P K C V R A K I Q D Y H I L T R K R I R Y R F R R F I Q Q F**  
211 **P Q C I R A K I Q D Y H I L T R K R I R Y R F R R F I Q Q F**  
~~S Q C K A T A R N L K L K Y L I N L E T L Q S A F Y T E F~~  
~~S Q C K A T A R N L K L K Y L I N L E T L Q S A F Y T E Q F~~  
250 260 270  
241 **S Q C K A T A R N L K L K Y L I N L E T L Q S A F Y T E Q F**  
241 **S O C K A T A R N L K L K Y L I N L E T L Q S A F Y T E K F**  
~~E V K E . . . G P S G E E I F A T I I I T G N G G I Q W S R~~  
~~E V K E S G S G P S G E E I F A T I I I T G N G G I Q W S R~~  
280 290 300  
271 **E V K E S A R G P S G E E I F A T I I I T G N G G I Q W S R**  
271 **E V K E P G S G P S G E E I F A T I I I T G N G G I Q W S R**  
~~G K H K E S E T L T E Q D Q L Y C D F P I I D V S I K Q~~  
~~G K H K E S E T L T E Q D V Q L Y C D F P D I I D V S I K Q~~  
310 320 330  
301 **G K H K E S E T L T E Q D V Q L Y C D F P D I I D V S I K Q**  
301 **G K H K E S E T L T E Q D L Q L Y C D F P N I I D V S I K Q**  
~~A N Q E S N E S R V T H K Q D G K L E I E L S S L~~  
~~A N Q E G S N E S R V V T V H K Q D G K V L E I E L S S L K~~  
340 350 360  
331 **A N Q E C S N E S R I V T V H K Q D G K V L E I E L S S L K**  
331 **A N Q E G S N E S R V V T I H K Q D G K N L E I E L S S L R**  
~~E A L S F V S L I D G Y Y R L T A D A H H Y L C K E V A P P~~  
~~E A L S F V S L I D G Y Y R L T A D A H H Y L C K E V A P P~~  
370 380 390  
361 **E A L S F V S L I D G Y Y R L T A D A H H Y L C K E V A P P**  
361 **E A L S F V S L I D G Y Y R L T A D A H H Y L C K E V A P P**

FIGURE 2B

~~AVLENI SNCHGPISMDFAISKLLKAGNOT~~  
~~AVLENIQSNCHGPISMDFAISKLLKAGNOT~~  
400 410 420  
391 **AVLENIH SNCHGPISMDFAISKLLKAGNOT**  
391 **AVLENIQ SNCHGPISMDFAISKLLKAGNOT**  
~~GLYVLRCS PKDFN KYFLTF AVERENVIEYK~~  
~~GLYVLRCS PKDFN KYFLTF AVERENVIEYK~~  
430 440 450  
421 **GLYVLRCS PKDFN KYFLTF AVERENVIEYK**  
421 **GLYVLRCS PKDFN KYFLTF AVERENVIEYK**  
~~HCLITKNEN EYNLSGT NPS LKDLLNC~~  
~~HCLITKNENGEYNLSGTNKNPSSSLKDLLNC~~  
460 470 480  
451 **HCLITKNENGEYNLSGTNRNPSNLKDLLNC**  
451 **HCLITKNENGEYNLSGTKKNPSNLKDLLNC**  
~~YQMETVRS DSIIFQFTKCCPPKPKDKSNLL~~  
~~YQMETVRS DSIIFQFTKCCPPKPKDKSNLL~~  
490 500 510  
481 **YQMETVRS DSIIFQFTKCCPPKPKDKSNLL**  
481 **YQMETVRS DSIIFQFTKCCPPKPKDKSNLL**  
~~VPR TNG SDV SPTLQR NQNVTHKI~~  
~~VPR TNGVSDVQISPTLQRHTNVNQHVT HKI~~  
520 530 540  
511 **VPR TNGI SDVQISPTLQRHNNV NQMVPHKI**  
511 **VPR TNGVSDVPT SPTLQRPTHM NQMVPHKI**  
~~RNEDLIFNESLGQGTFTKIFKGVRRREVGDY~~  
~~RNEDLIFNESLGQGTFTKIFKGVRRREVGDY~~  
550 560 570  
541 **RNEDLIFNESLGQGTFTKIFKGVRRREVGDY**  
541 **RNEDLIFNESLGQGTFTKIFKGVRRREVGDY**  
~~GQLH TEVLLKVLDKAHRNYSSESFFEAASM~~  
~~GQLHETEVL LKVLDKAHRNYSSESFFEAASM~~  
580 590 600  
571 **GQLHETEVL LKVLDKAHRNYSSESFFEAASM**  
571 **GQLHETEVL LKVLDKAHRNYSSESFFEAASM**

FIGURE 2C

MS LSHKHLVLNYGVGVCG ENILVQEFVK  
MSQLSHKHLVLNYGVGVCGDENILVQEFVK

610 620 630

601 MSQ LSHKHLVLNYGVGVCGE ENILVQEFVK  
601 MSK LSHKHLVLNYGVGVCGD ENILVQEFVK

FGSLDITYLKKNKN INILWKL VAKQLAWA  
FGSLDITYLKKNKNSINILWKLGVAKQLAWA

640 650 660

631 FGSLDITYLKKNKNS INILWKLGVAKQLAWA  
631 FGSLDITYLKKNKNC INILWKLGVAKQLAWA

MHFLEE LIHGNVCAKNILLIREEDR TG  
MHFLEENSLIHGNVCAKNILLIREEDRKTG

670 680 690

661 MHFLEEKS LIHGNVCAKNILLIREEDRRTG  
661 MHFLEENT LIHGNVCAKNILLIREEDRKTG

NPPFIKLSDPGISITVLPKDILOERIPWVP  
NPPFIKLSDPGISITVLPKDILOERIPWVP

700 710 720

691 NPPFIKLSDPGISITVLPKDILOERIPWVP  
691 NPPFIKLSDPGISITVLPKDILOERIPWVP

PECIENPKNLNLATDKWSFGTTLWEICSGG  
PECIENPKNLNLATDKWSFGTTLWEICSGG

730 740 750

721 PECIENPKNLNLATDKWSFGTTLWEICSGG  
721 PECIENPKNLNLATDKWSFGTTLWEICSGG

DKPLSALDSQRKLQFYED HQLPAPKW EL  
DKPLSALDSQRKLQFYEDKHQLPAPKWAEL

760 770 780

751 DKPLSALDSQRKLQFYEDKHQLPAPKWTEL  
751 DKPLSALDSQRKLQFYEDRHQLPAPKWAEL

ANLINNCMDYEPDFRP FRA IRLNSLFT  
ANLINNCMDYEPDFRP AFRAVIRDLNSLFT

790 800 810

781 ANLINNCMDYEPDFRP AFRAVIRDLNSLFT  
781 ANLINNCMDYEPDFRP SPRAIIRDLNSLFT

FIGURE 2D

~~P D Y E L L T E N D M L P N M R I G A L G F S G A F E D R D~~  
~~P D Y E L L T E N D M L P N M R I G A L G F S G A F E D R D~~  
820 830 840  
811 **P D Y E L L T E N D M L P N M R I G A L G F S G A F E D R D**  
811 **P D Y E L L T E N D M L P N M R I G A L G F S G A F E D R D**

~~P T Q F E E R H L K F L Q Q L G K G N F G S V E M C R Y D P~~  
~~P T Q F E E R H L K F L Q Q L G K G N F G S V E M C R Y D P~~  
850 860 870  
841 **P T Q F E E R H L K F L Q Q L G K G N F G S V E M C R Y D P**  
841 **P T Q F E E R H L K F L Q Q L G K G N F G S V E M C R Y D P**

~~L Q D N T G E V V A V K K L Q H S T E E H L R D F E R E I E~~  
~~L Q D N T G E V V A V K K L Q H S T E E H L R D F E R E I E~~  
880 890 900  
871 **L Q D N T G E V V A V K K L Q H S T E E H L R D F E R E I E**  
871 **L Q D N T G E V V A V K K L Q H S T E E H L R D F E R E I E**

~~I L K S L Q H D N I V K Y K G V C Y S A G R R N L K L I M E~~  
~~I L K S L Q H D N I V K Y K G V C Y S A G R R N L K L I M E~~  
910 920 930  
901 **I L K S L Q H D N I V K Y K G V C Y S A G R R N L R L I M E**  
901 **I L K S L Q H D N I V K Y K G V C Y S A G R R N L K L I M E**

~~Y L P Y G S L R D Y L Q K H K E R I D H K L L Q Y T S Q I~~  
~~Y L P Y G S L R D Y L Q K H K E R I D H K L L Q Y T S Q I~~  
940 950 960  
931 **Y L P Y G S L R D Y L Q K H K E R I D H K L L Q Y T S Q I**  
931 **Y L P Y G S L R D Y L Q K H K E R I D H K L L Q Y T S Q I**

~~C K G M E Y L G T K R Y I H R D L A T R N I L V E N E N R V~~  
~~C K G M E Y L G T K R Y I H R D L A T R N I L V E N E N R V~~  
970 980 990  
951 **C K G M E Y L G T K R Y I H R D L A T R N I L V E N E N R V**  
961 **C K G M E Y L G T K R Y I H R D L A T R N I L V E N E N R V**

~~K I G D F G L T K V L P O D K E Y Y K V K E P G E S P I F W~~  
~~K I G D F G L T K V L P O D K E Y Y K V K E P G E S P I F W~~  
1000 1010 1020  
991 **K I G D F G L T K V L P O D K E Y Y K V K E P G E S P I F W**  
991 **K I G D F G L T K V L P O D K E Y Y K V K E P G E S P I F W**

FIGURE 2E

~~Y A P . S L T E S K F S V A S D V W S F G V V L Y E L F T Y~~  
~~Y A P E S L T E S K F S V A S D V W S F G V V L Y E L F T Y~~  
1030 1040 1050  
1021 **Y A P Q S L T E S K F S V A S D V W S F G V V L Y E L F T Y**  
1021 **Y A P E S L T E S K F S V A S D V W S F G V V L Y E L F T Y**  
~~I E K S K S P P . E F M R M I G N D K Q G Q M I V F H L I E~~  
~~I E K S K S P P A E F M R M I G N D K Q G Q M I V F H L I E~~  
1060 1070 1080  
1051 **I E K S K S P P V E F M R M I G N D K Q G Q M I V F H L I E**  
1051 **I E K S K S P P A E F M R M I G N D K Q G Q M I V F H L I E**  
~~L L K . N G R L P R P . G C P D E I Y . I M T E C W N N N V~~  
~~L L K S N G R L P R P D G C P D E I Y V I M T E C W N N N V~~  
1090 1100 1110  
1081 **L L K S N G R L P R P E G C P D E I Y V I M T E C W N N N V**  
1081 **L L K N N G R L P R P D G C P D E I Y M I M T E C W N N N V**  
~~Q R P S F R D L . I~~  
~~S Q R P S F R D L A L R V G Q I K D G T A G~~  
1120 1130  
1111 **S Q R P S F R D L S F - - G W I K C G T V**  
1111 **N Q R P S F R D L A L R V D Q I R D N M A G**

FIGURE 2F